Table S1. Bacterial strains and plasmids used in this study.

Strain or plasmid	Relevant genotype or phenotype	Source or reference
Strains		
E. coli		
TOP10	Chemically competent cells	Invitrogen
BL21 Star (DE3)	F^-*ompT hsdS*$_B$ ($r_B^-m_B^-$)*gal dcm rne131* (DE3)	Invitrogen
P. aeruginosa		
CHA	Mucoid CF isolate	(1)
CHAΔ*pcrV*	CHA with an internal deletion of the *pcrV* gene	(2)
Plasmids		
pTOPO	Kn^R	Invitrogen
pET-Duet1	Ap^R	Novagen
pET-Duet1-*pcr*V	Ap^R	*This study*
pET-Duet1-*pcrVdeltaCer*	Ap^R	*This study*
pIA60	7-kb *Eco*RI fragment from CHA with *pcrGVH-popBD* and *exsCEBA* in pUC18	(2)
pIApG	Ap^R, transcriptional fusion between promoter of *pcrGVHpopBD* (pG) and *gfpmut3* gene	(2)
pIApG-*pcr*V	Ap^R, *Xba*I/*Hin*dIII fragment of *pcrV* into pIApG	(2)
pIApG-*pcrVdeltaCter*	Ap^R, *Xba*I/*Hin*dIII fragment of *pcrVΔCter* into pIApG	*This study*

Table S2. Oligonucleotides used in this study.

Primer	DNA sequence [a]
Cloning	
CG_VNdeI	5' ACATATGGAAGTCAGAAACCTTAA 3'
CG_VAatII	5' AGACGTCTAGATCGCGCTGAGAATG 3'
CG_VXbaI	5' ATCTAGAATCTGAGGAATCACGATG 3'
CG_VHindIII	5' AAAGCTTGATCGCGCTGAGAATGTC 3'
CG_deltaVAatII	5' AGACGTCTCAGTCGTCAGCGGACGC 3'
CG_deltaVHindIII	5' AAAGCTTTCAGTCGTTCAGCGGACGC 3'
Site directed mutagenesis	
L262A_sens	5' GAGAAGACCACCCTGGCGAACGACACCAGCTCC 3'
L262A_as	5' GGAGTCGGTGTCGTTCGCCAGGGTGGTCTTCTC 3'
L262D_sens	5' GAGAAGACCACCCTGGACAACGACACCAGCTCC 3'
L262D_as	5' GGAGTCGGTGTCGTTGTCCAGGGTGGTCTTCTC 3'
CG_msPcrV_L276A	5' TCGGCGGTCGAGGCGGCCAACCGCTTCATCCAG 3'
CG_masPcrV_L276A	5' CTGGATGAAGCGGTTGGCCGCCTCGACCGCCGA 3'
L276D_sens	5' CTGGATGAAGCGGTTGGCCGCCTCGACCGCCGA 3'
L276D_as	5' CTGGATGAAGCGGTTGTCCGCCTCGACCGCCGA 3'
CG_msPcrV_R278A	5' CGAGGCGCTCAACGCCTTCATCCAGAAATACG 3'
CG_masPcrV_R278A	5' CGTATTTCTGGATGAAGGCGTTGAGCGCCTCG 3'
CG_msPcrV_F279A	5' TCGAGGCGCTCAACCGCGCCATCCAGAAATACGACAG 3'
CG_masPcrV_F279A	5' TCGAGGCGCTCAACCGCGCCATCCAGAAATACGACAG 3'
CG_msPcrV_Y283A	5' CTGTCGTATTTCTGGATGGCGCGGTTGAGCGCCTCGA 3'
CG_masPcrV_Y283A	5' ACCGCTTCATCCAGAAAGCCGACAGCGTCCTGCGCGAC3'
CG_msPcrV_D284A	5' GTCGCGCAGGACGCTGTCGGCTTTCTGGATGAAGCGGT 3'
CG_masPcrV_D284A	5' CATCCAGAAATACGCCAGCGTCCTGCGCG 3'
CG_msPcrV_V286A	5' CGCGCAGGACGCTGGCGTATTTCTGGATG 3'
CG_masPcrV_V286A	5' TCCAGAAATACGACAGCGCCCTGCGCGACATTCTCAG 3'
CG_msPcrV_R288A	5' CTGAGAATGTCGCGCAGGGCGCTGTCGTATTTCTGGA 3'
CG_masPcrV_R288A	5' CGACAGCGTCCTGGCCGACATTCTCAGCGCG 3'
CG_msPcrV_I290A	5' CGCGCTGAGAATGTCGGCCAGGACGCTGTCG 3'
CG_masPcrV_I290A	5' ACAGCGTCCTGCGCGACGCCCTCAGCGCGATCTAGAC 3'
	5' GTCTAGATCGCGCTGAGGGCGTCGCGCAGGACGCTGT 3'

[a] Restriction sites or mismatching bases incorporated into primers are underlined.

References

1. Toussaint, B., Delic-Attree, I., and Vignais, P. M. (1993) *Biochem. Biophys. Res. Commun.* **196**, 416-421
2. Goure, J., Pastor, A., Faudry, E., Chabert, J., Dessen, A., and Attree, I. (2004) *Infect. Immun.* **72**, 4741-4750